

RAW SEQUENCE LISTING

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Application Serial Number: 10/595,840
Source: IFWO
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DATE: 05/24/2006

PATENT APPLICATION: US/10/595,840

TIME: 15:51:30

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\05242006\J595840.raw

3 <110> APPLICANT: JEROME, Keith R.
 4 SLOAN, Derek D.
 6 <120> TITLE OF INVENTION: METHODS FOR SCREENING FOR AGENTS CAPABLE OF MODULATING T
 LYMPHOCYTE
 7 FUNCTION IN RESPONSE TO A HERPES SIMPLEX VIRUS-INFECTED CELL
 9 <130> FILE REFERENCE: 14538A-008110US
 11 <140> CURRENT APPLICATION NUMBER: 10/595,840
 12 <141> CURRENT FILING DATE: 2006-05-15
 14 <150> PRIOR APPLICATION NUMBER: PCT/US2004/038050
 15 <151> PRIOR FILING DATE: 2004-11-15
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 481
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Herpes simplex virus 1
 26 <400> SEQUENCE: 1
 28 Met Ala Cys Arg Lys Phe Cys Arg Val Tyr Gly Gly Gln Gly Arg Arg
 29 1 5 10 15
 32 Lys Glu Glu Ala Val Pro Pro Glu Thr Lys Pro Ser Arg Val Phe Pro
 33 20 25 30
 36 His Gly Pro Phe Tyr Thr Pro Ala Glu Asp Ala Cys Leu Asp Ser Pro
 37 35 40 45
 40 Pro Pro Glu Thr Pro Lys Pro Ser His Thr Thr Pro Pro Ser Glu Ala
 41 50 55 60
 44 Glu Arg Leu Cys His Leu Gln Glu Ile Leu Ala Gln Met Tyr Gly Asn
 45 65 70 75 80
 48 Gln Asp Tyr Pro Ile Glu Asp Asp Pro Ser Ala Asp Ala Ala Asp Asp
 49 85 90 95
 52 Val Asp Glu Asp Ala Pro Asp Asp Val Ala Tyr Pro Glu Glu Tyr Ala
 53 100 105 110
 56 Glu Glu Leu Phe Leu Pro Gly Asp Ala Thr Gly Pro Leu Ile Gly Ala
 57 115 120 125
 60 Asn Asp His Ile Pro Pro Pro Cys Gly Ala Ser Pro Pro Gly Ile Arg
 61 130 135 140
 64 Arg Arg Ser Arg Asp Glu Ile Gly Ala Thr Gly Phe Thr Ala Glu Glu
 65 145 150 155 160
 68 Leu Asp Ala Met Asp Arg Glu Ala Ala Arg Ala Ile Ser Arg Gly Gly
 69 165 170 175
 72 Lys Pro Pro Ser Thr Met Ala Lys Leu Val Thr Gly Met Gly Phe Thr
 73 180 185 190
 76 Ile His Gly Ala Leu Thr Pro Gly Ser Glu Gly Cys Val Phe Asp Ser
 77 195 200 205
 80 Ser His Pro Asp Tyr Pro Gln Arg Val Ile Val Lys Ala Gly Trp Tyr

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81      210      215      220
84 Thr Ser Thr Ser His Glu Ala Arg Leu Leu Arg Arg Leu Asp His Pro
85 225      230      235      240
88 Ala Ile Leu Pro Leu Leu Asp Leu His Val Val Ser Gly Val Thr Cys
89      245      250      255
92 Leu Val Leu Pro Lys Tyr Gln Ala Asp Leu Tyr Thr Tyr Leu Ser Arg
93      260      265      270
96 Arg Leu Asn Pro Leu Gly Arg Pro Gln Ile Ala Ala Val Ser Arg Gln
97      275      280      285
100 Leu Leu Ser Ala Val Asp Tyr Ile His Arg Gln Gly Ile Ile His Arg
101      290      295      300
104 Asp Ile Lys Thr Glu Asn Ile Phe Ile Asn Thr Pro Glu Asp Ile Cys
105 305      310      315      320
108 Leu Gly Asp Phe Gly Ala Ala Cys Phe Val Gln Gly Ser Arg Ser Ser
109      325      330      335
112 Pro Phe Pro Tyr Gly Ile Ala Gly Thr Ile Asp Thr Asn Ala Pro Glu
113      340      345      350
116 Val Leu Ala Gly Asp Pro Tyr Thr Thr Thr Val Asp Ile Trp Ser Ala
117      355      360      365
120 Gly Leu Val Ile Phe Glu Thr Ala Val His Asn Ala Ser Leu Phe Ser
121      370      375      380
124 Ala Pro Arg Gly Pro Lys Arg Gly Pro Cys Asp Ser Gln Ile Thr Arg
125 385      390      395      400
128 Ile Ile Arg Gln Ala Gln Val His Val Asp Glu Phe Ser Pro His Pro
129      405      410      415
132 Glu Ser Arg Leu Thr Ser Arg Tyr Arg Ser Arg Ala Ala Gly Asn Asn
133      420      425      430
136 Arg Pro Pro Tyr Thr Arg Pro Ala Trp Thr Arg Tyr Tyr Lys Met Asp
137      435      440      445
140 Ile Asp Val Glu Tyr Leu Val Cys Lys Ala Leu Thr Phe Asp Gly Ala
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144 Leu Arg Pro Ser Ala Ala Glu Leu Leu Cys Leu Pro Leu Phe Gln Gln
145 465      470      475      480
148 Lys
152 <210> SEQ ID NO: 2
153 <211> LENGTH: 481
154 <212> TYPE: PRT
155 <213> ORGANISM: Herpes simplex virus 2
157 <400> SEQUENCE: 2
159 Met Ala Cys Arg Lys Phe Cys Gly Val Tyr Arg Arg Pro Asp Lys Arg
160 1      5      10      15
163 Gln Glu Ala Ser Val Pro Pro Glu Thr Asn Thr Ala Pro Ala Phe Pro
164      20      25      30
167 Ala Ser Thr Phe Tyr Thr Pro Ala Glu Asp Ala Tyr Leu Ala Pro Gly
168      35      40      45
171 Pro Pro Glu Thr Ile His Pro Ser Arg Pro Pro Ser Pro Gly Glu Ala
172      50      55      60
175 Ala Arg Leu Cys Gln Leu Gln Glu Ile Leu Ala Gln Met His Ser Asp
176 65      70      75      80

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179 Glu Asp Tyr Pro Ile Val Asp Ala Ala Gly Ala Glu Glu Glu Asp Glu
180      85      90      95
183 Ala Asp Asp Asp Ala Pro Asp Asp Val Ala Tyr Pro Glu Asp Tyr Ala
184      100     105     110
187 Glu Gly Arg Phe Leu Ser Met Val Ser Ala Ala Pro Leu Pro Gly Ala
188      115     120     125
191 Ser Gly His Pro Pro Val Pro Gly Arg Ala Ala Pro Pro Asp Val Arg
192      130     135     140
195 Thr Cys Asp Thr Gly Lys Val Gly Ala Thr Gly Phe Thr Pro Glu Glu
196 145      150     155     160
199 Leu Asp Thr Met Asp Arg Glu Ala Leu Arg Ala Ile Ser Arg Gly Cys
200      165     170     175
203 Lys Pro Pro Ser Thr Leu Ala Lys Leu Val Thr Gly Leu Gly Phe Ala
204      180     185     190
207 Ile His Gly Ala Leu Ile Pro Gly Ser Glu Gly Cys Val Phe Asp Ser
208      195     200     205
211 Ser His Pro Asn Tyr Pro His Arg Val Ile Val Lys Ala Gly Trp Tyr
212      210     215     220
215 Ala Ser Thr Ser His Glu Ala Arg Leu Leu Arg Arg Leu Asn His Pro
216 225      230     235     240
219 Ala Ile Leu Pro Leu Leu Asp Leu His Val Val Ser Gly Val Thr Cys
220      245     250     255
223 Leu Val Leu Pro Lys Tyr His Cys Asp Leu Tyr Thr Tyr Leu Ser Lys
224      260     265     270
227 Arg Pro Ser Pro Leu Gly His Leu Gln Ile Thr Ala Val Ser Arg Gln
228      275     280     285
231 Leu Leu Ser Ala Ile Asp Tyr Val His Cys Lys Gly Ile Ile His Arg
232      290     295     300
235 Asp Ile Lys Thr Glu Asn Ile Phe Ile Asn Thr Pro Glu Asn Ile Cys
236 305      310     315     320
239 Leu Gly Asp Phe Gly Ala Ala Cys Phe Val Arg Gly Cys Arg Ser Ser
240      325     330     335
243 Pro Phe His Tyr Gly Ile Ala Gly Thr Ile Asp Thr Asn Ala Pro Glu
244      340     345     350
247 Val Leu Ala Gly Asp Pro Tyr Thr Gln Val Ile Asp Ile Trp Ser Ala
248      355     360     365
251 Gly Leu Val Ile Phe Glu Thr Ala Val His Thr Ala Ser Leu Phe Ser
252      370     375     380
255 Ala Pro Arg Asp Pro Glu Arg Arg Pro Cys Asp Asn Gln Ile Ala Arg
256 385      390     395     400
259 Ile Ile Arg Gln Ala Gln Val His Val Asp Glu Phe Pro Thr His Ala
260      405     410     415
263 Glu Ser Arg Leu Thr Ala His Tyr Arg Ser Arg Ala Ala Gly Asn Asn
264      420     425     430
267 Arg Pro Ala Trp Thr Arg Pro Ala Trp Thr Arg Tyr Tyr Lys Ile His
268      435     440     445
271 Thr Asp Val Glu Tyr Leu Ile Cys Lys Ala Leu Thr Phe Asp Ala Ala
272      450     455     460
275 Leu Arg Pro Ser Ala Ala Glu Leu Leu Arg Leu Pro Leu Phe His Pro

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/595,840

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